Minimizing metabolic burden caused by heterologous expression of synthetic pathways in *E. coli*: identification of stress sensors

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Advances in synthetic biology and metabolic engineering have established the beginnings of a technological transition in the chemical manufacturing industry towards a bio-based industry that creates chemicals from renewable resources. The biotechnological production of complex chemicals, secondary plant metabolites for instance, requires the heterologous expression of multi-gene pathways in production hosts such as *E. coli*.

The traditional metabolic engineering approach to the optimization of the flux through these pathways consists of massively overexpressing the enzymes involved. This does not, however, take into account the effect of the heterologous pathway on the host metabolism. As such, it often leads to suboptimal solutions with low productivity due to a significant metabolic burden caused on the one hand by the withdrawal of biomass precursors from the central metabolism and the accumulation of toxic intermediates on the other hand.

This research project aims to identify native *E. coli* promoters that become active in the presence of a number of stress conditions, for instance the *IbpAB* promoter that responds to the formation of inclusion bodies. To this effect, a set of genetic constructs has been created in which multiple promoters and stress inducing genes are to be cloned to enable a modular stress sensor assay.